

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Murphy, Patricia D.  
Allen, Antonette C.  
Alvares, Christopher P.  
Critz, Brenda S.  
Olson, Sheri J.  
Schelter, Denise B.  
Zeng, Bin
- (ii) TITLE OF INVENTION: A Sequence of the Human BRCA1 Gene
- (iii) NUMBER OF SEQUENCES: 78
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: ONCORMED  
(B) STREET: 200 PERRY PARKWAY  
(C) CITY: GAITHERSBURG  
(D) STATE: MD  
(E) COUNTRY: USA  
(F) ZIP: 20877
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: to be assigned  
(B) FILING DATE: herewith  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: R. THOMAS GALLEGOS  
(B) REGISTRATION NUMBER: 32,692

(C) REFERENCE/DOCKET NUMBER: PA-0054

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5711 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(B) STRAIN: BRCA1

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: 17

(B) MAP POSITION: 17q21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCTCGCTGA GACTTCCTGG ACCCCGCACC AGGCTGTGGG GTTCTCAGA TAACTGGGCC	60
CCTGCGCTCA GGAGGCCTTC ACCCTCTGCT CTGGGTAAAG TTCATTGGAA CAGAAAGAAA	120
TGGATTTATC TGCTCTTCGC GTTGAAGAAG TACAAAATGT CATTAATGCT ATGCAGAAAA	180
TCTTAGAGTG TCCCATCTGT CTGGAGTTGA TCAAGGAACC TGTCTCCACA AAGTGTGACC	240
ACATATTTTG CAAATTTTGC ATGCTGAAAC TTCTCAACCA GAAGAAAGGG CCTTCACAGT	300

GTCCTTTATG TAAGAATGAT ATAACCAAAA GGAGCCTACA AGAAAGTACG AGATTTAGTC	360
AACTTGTTGA AGAGCTATTG AAAATCATTG GTGCTTTTCA GCTTGACACA GGTTCGGAGT	420
ATGCAAACAG CTATAATTTT GCAAAAAAGG AAAATAACTC TCCTGAACAT CTAAAAGATG	480
AAGTTTCTAT CATCCAAAGT ATGGGCTACA GAAACCGTGC CAAAAGACTT CTACAGAGTG	540
AACCCGAAAA TCCTTCCTTG CAGGAAACCA GTCTCAGTGT CCAACTCTCT AACCTTGGA	600
CTGTGAGAAC TCTGAGGACA AAGCAGCGGA TACAACCTCA AAAGACGTCT GTCTACATTG	660
AATTGGGATC TGATTCTTCT GAAGATACCG TTAATAAGGC AACTTATTGC AGTGTGGGAG	720
ATCAAGAATT GTTACAAATC ACCCCTCAAG GAACCAGGGA TGAAATCAGT TTGGATTCTG	780
CAAAAAAGGC TGCTTGTAAG TTTTCTGAGA CGGATGTAAC AAATACTGAA CATCATCAAC	840
CCAGTAATAA TGATTTGAAC ACCACTGAGA AGCGTGCAGC TGAGAGGCAT CCAGAAAAGT	900
ATCAGGGTAG TTCTGTTTCA AACTTGCAATG TGGAGCCATG TGGCACAAAT ACTCATGCCA	960
GCTCATTACA GCATGAGAAC AGCAGTTTAT TACTCACTAA AGACAGAATG AATGTAGAAA	1020
AGGCTGAATT CTGTAATAAA AGCAACAGC CTGGCTTAGC AAGGAGCCAA CATAACAGAT	1080
GGGCTGGAAG TAAGGAAACA TGTAATGATA GCGGACTCC CAGCACAGAA AAAAAGGTAG	1140
ATCTGAATGC TGATCCCCTG TGTGAGAGAA AAGAATGGAA TAAGCAGAAA CTGCCATGCT	1200
CAGAGAATCC TAGAGATACT GAAGATGTTT CTTGGATAAC ACTAAATAGC AGCATTGAGA	1260
AAGTTAATGA GTGGTTTTC AGAAGTGATG AACTGTTAGG TTCTGATGAC TCACATGATG	1320
GGGAGTCTGA ATCAAATGCC AAAGTAGCTG ATGTATTGGA CGTTCTAAAT GAGGTAGATG	1380
AATATTCTGG TTCTTCAGAG AAAATAGACT TACTGGCCAG TGATCCTCAT GAGGCTTTAA	1440
TATGTAAAAG TGAAAGAGTT CACTCCAAAT CAGTAGAGAG TAATATTGAA GACAAAATAT	1500

TTGGGAAAAC CTATCGGAAG AAGGCAAGCC TCCCCAACTT AAGCCATGTA ACTGAAAATC	1560
TAATTATAGG AGCATTGTGTT ACTGAGCCAC AGATAATACA AGAGCGTCCC CTCACAAATA	1620
AATTAAAGCG TAAAAGGAGA CCTACATCAG GCCTTCATCC TGAGGATTTT ATCAAGAAAG	1680
CAGATTGCGC AGTTCAAAAG ACTCCTGAAA TGATAAATCA GGGAACTAAC CAAACGGAGC	1740
AGAATGGTCA AGTGATGAAT ATTACTAATA GTGGTCATGA GAATAAAACA AAAGGTGATT	1800
CTATTCAGAA TGAGAAAAAT CCTAACCCAA TAGAATCACT CGAAAAAGAA TCTGCTTTCA	1860
AAACGAAAGC TGAACCTATA AGCAGCAGTA TAAGCAATAT GGAACCTCGAA TTAAATATCC	1920
ACAATTCAAA AGCACCTAAA AAGAATAGGC TGAGGAGGAA GTCTTCTACC AGGCATATTC	1980
ATGCGCTTGA ACTAGTAGTC AGTAGAAATC TAAGCCCACC TAATTGTACT GAATTGCAAA	2040
TTGATAGTTG TTCTAGCAGT GAAGAGATAA AGAAAAAAAA GTACAACCAA ATGCCAGTCA	2100
GGCACAGCAG AAACCTACAA CTCATGGAAG GTAAAGAACC TGCAACTGGA GCCAAGAAGA	2160
GTAACAAGCC AAATGAACAG ACAAGTAAAA GACATGACAG TGATACTTTC CCAGAGCTGA	2220
AGTTAACAAA TGCACCTGGT TCTTTTACTA AGTGTTCAAA TACCAGTGAA CTTAAAGAAT	2280
TTGTCAATCC TAGCCTTCCA AGAGAAGAAA AAGAAGAGAA ACTAGAAACA GTTAAAGTGT	2340
CTAATAATGC TGAAGACCCC AAAGATCTCA TGTTAAGTGG AGAAAGGGTT TTGCAAACCTG	2400
AAAGATCTGT AGAGAGTAGC AGTATTTTAC TGGTACCTGG TACTGATTAT GGCACCTCAGG	2460
AAAGTATCTC GTTACTGGAA GTTAGCACTC TAGGGAAGGC AAAAACAGAA CCAAATAAAT	2520
GTGTGAGTCA GTGTGCAGCA TTTGAAAACC CCAAGGGACT AATTCATGGT TGTTCCAAAG	2580
ATAATAGAAA TGACACAGAA GGCTTTAAGT ATCCATTGGG ACATGAAGTT AACCACAGTC	2640
GGGAAACAAG CATAGAAATG GAAGAAAGTG AACTTGATGC TCAGTATTTG CAGAATACAT	2700

TCAAGGTTTC	AAAGCGCCAG	TCATTTGCTC	TGTTTTCAAA	TCCAGGAAAT	GCAGAAGAGG	2760
AATGTGCAAC	ATTCTCTGCC	CACTCTGGGT	CCTTAAAGAA	ACAAAGTCCA	AAAGTCACTT	2820
TTGAATGTGA	ACAAAAGGAA	GAAAATCAAG	GAAAGAATGA	GTCTAATATC	AAGCCTGTAC	2880
AGACAGTTAA	TATCACTGCA	GGCTTTCCTG	TGGTTGGTCA	GAAAGATAAG	CCAGTTGATA	2940
ATGCCAAATG	TAGTATCAAA	GGAGGCTCTA	GGTTTTGTCT	ATCATCTCAG	TTCAGAGGCA	3000
ACGAAACTGG	ACTCATTACT	CCAAATAAAC	ATGGACTTTT	ACAAAACCCA	TATCGTATAC	3060
CACCACTTTT	TCCCATCAAG	TCATTTGTTA	AAACTAAATG	TAAGAAAAAT	CTGCTAGAGG	3120
AAAACTTTGA	GGAACATTCA	ATGTCACCTG	AAAGAGAAAT	GGGAAATGAG	AACATTCCAA	3180
GTACAGTGAG	CACAATTAGC	CGTAATAACA	TTAGAGAAAA	TGTTTTTAAA	GGAGCCAGCT	3240
CAAGCAATAT	TAATGAAGTA	GGTTCAGTA	CTAATGAAGT	GGGCTCCAGT	ATTAATGAAA	3300
TAGGTTCAG	TGATGAAAAC	ATTCAAGCAG	AACTAGGTAG	AAACAGAGGG	CCAAAATTGA	3360
ATGCTATGCT	TAGATTAGGG	GTTTTGCAAC	CTGAGGTCTA	TAAACAAAGT	CTTCCTGGAA	3420
GTAATTGTAA	GCATCCTGAA	ATAAAAAAGC	AAGAATATGA	AGAAGTAGTT	CAGACTGTTA	3480
ATACAGATTT	CTCTCCATAT	CTGATTTTCT	ATAACTTAGA	ACAGCCTATG	GGAAGTAGTC	3540
ATGCATCTCA	GGTTTGTTCT	GAGACACCTG	ATGACCTGTT	AGATGATGGT	GAAATAAAGG	3600
AAGATACTAG	TTTTGCTGAA	AATGACATTA	AGGAAAGTTC	TGCTGTTTTT	AGCAAAAGCG	3660
TCCAGAGAGG	AGAGCTTAGC	AGGAGTCCTA	GCCCTTTCAC	CCATACACAT	TTGGCTCAGG	3720
GTTACCGAAG	AGGGGCCAAG	AAATTAGAGT	CCTCAGAAGA	GAACCTATCT	AGTGAGGATG	3780
AAGAGCTTCC	CTGCTTCCAA	CACTTGTTAT	TTGGTAAAGT	AAACAATATA	CCTTCTCAGT	3840
CTACTAGGCA	TAGCACCGTT	GCTACCGAGT	GTCTGTCTAA	GAACACAGAG	GAGAATTTAT	3900

TATCATTGAA	GAATAGCTTA	AATGACTGCA	GTAACCAGGT	AATATTGGCA	AAGGCATCTC	3960
AGGAACATCA	CCTTAGTGAG	GAAACAAAAT	GTTCTGCTAG	CTTGTTTTCT	TCACAGTGCA	4020
GTGAATTGGA	AGACTTGACT	GCAAATACAA	ACACCCAGGA	TCCTTTCTTG	ATTGGTTCTT	4080
CCAAACAAAT	GAGGCATCAG	TCTGAAAGCC	AGGGAGTTGG	TCTGAGTGAC	AAGGAATTGG	4140
TTTCAGATGA	TGAAGAAAGA	GGAACGGGCT	TGGAAGAAAA	TAATCAAGAA	GAGCAAAGCA	4200
TGGATTCAAA	CTTAGGTGAA	GCAGCATCTG	GGTGTGAGAG	TGAAACAAGC	GTCTCTGAAG	4260
ACTGCTCAGG	GCTATCCTCT	CAGAGTGACA	TTTAAACCAC	TCAGCAGAGG	GATACCATGC	4320
AACATAACCT	GATAAAGCTC	CAGCAGGAAA	TGGCTGAACT	AGAAGCTGTG	TTAGAACAGC	4380
ATGGGAGCCA	GCCTTCTAAC	AGCTACCCTT	CCATCATAAG	TGACTCCTCT	GCCCTTGAGG	4440
ACCTGCGAAA	TCCAGAACAA	AGCACATCAG	AAAAAGCAGT	ATTAACCTCA	CAGAAAAGTA	4500
GTGAATACCC	TATAAGCCAG	AATCCAGAAG	GCCTTTCTGC	TGACAAGTTT	GAGGTGTCTG	4560
CAGATAGTTC	TACCAGTAAA	AATAAAGAAC	CAGGAGTGGA	AAGGTCATCC	CCTTCTAAAT	4620
GCCCATCATT	AGATGATAGG	TGGTACATGC	ACAGTTGCTC	TGGGAGTCTT	CAGAATAGAA	4680
ACTACCCATC	TCAAGAGGAG	CTCATTAAGG	TTGTTGATGT	GGAGGAGCAA	CAGCTGGAAG	4740
AGTCTGGGCC	ACACGATTTG	ACGGAAACAT	CTTACTTGCC	AAGGCAAGAT	CTAGAGGGAA	4800
CCCCTTACCT	GGAATCTGGA	ATCAGCCTCT	TCTCTGATGA	CCCTGAATCT	GATCCTTCTG	4860
AAGACAGAGC	CCCAGAGTCA	GCTCGTGTTG	GCAACATACC	ATCTTCAACC	TCTGCATTGA	4920
AAGTTCCCCA	ATTGAAAGTT	GCAGAATCTG	CCCAGGGTCC	AGCTGCTGCT	CATACTACTG	4980
ATACTGCTGG	GTATAATGCA	ATGGAAGAAA	GTGTGAGCAG	GGAGAAGCCA	GAATTGACAG	5040
CTTCAACAGA	AAGGGTCAAC	AAAAGAATGT	CCATGGTGGT	GTCTGGCCTG	ACCCCAAGAAG	5100

AATTTATGCT	CGTGACAAG	TTTGCCAGAA	AACACCACAT	CACTTTAACT	AATCTAATTA	5160
CTGAAGAGAC	TACTCATGTT	GTTATGAAAA	CAGATGCTGA	GTTTGTGTGT	GAACGGACAC	5220
TGAAATATTT	TCTAGGAATT	GCGGGAGGAA	AATGGGTAGT	TAGCTATTTT	TGGGTGACCC	5280
AGTCTATTAA	AGAAAGAAAA	ATGCTGAATG	AGCATGATTT	TGAAGTCAGA	GGAGATGTGG	5340
TCAATGGAAG	AAACCACCAA	GGTCCAAAGC	GAGCAAGAGA	ATCCCAGGAC	AGAAAGATCT	5400
TCAGGGGGCT	AGAAATCTGT	TGCTATGGGC	CCTTCACCAA	CATGCCCACA	GATCAACTGG	5460
AATGGATGGT	ACAGCTGTGT	GGTGCTTCTG	TGGTGAAGGA	GCTTTCATCA	TTCACCCTTG	5520
GCACAGGTGT	CCACCCAATT	GTGGTTGTGC	AGCCAGATGC	CTGGACAGAG	GACAATGGCT	5580
TCCATGCAAT	TGGGCAGATG	TGTGAGGCAC	CTGTGGTGAC	CCGAGAGTGG	GTGTTGGACA	5640
GTGTAGCACT	CTACCAGTGC	CAGGAGCTGG	ACACCTACCT	GATACCCCAG	ATCCCCCACA	5700
GCCACTACTG	A					5711

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1863 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (B) STRAIN: BRCA1

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: 17
- (B) MAP POSITION: 17q21

Met Asp Leu Ser Ala Leu Arg Val Glu Glu Val Gln Asn Val Ile Asn  
1 5 10 15

Ala Met Gln Lys Ile Leu Glu Cys Pro Ile Cys Leu Glu Leu Ile Lys  
20 25 30

Glu Pro Val Ser Thr Lys Cys Asp His Ile Phe Cys Lys Phe Cys Met  
35 40 45

Leu Lys Leu Leu Asn Gln Lys Lys Gly Pro Ser Gln Cys Pro Leu Cys  
50 55 60

Lys Asn Asp Ile Thr Lys Arg Ser Leu Gln Glu Ser Thr Arg Phe Ser  
65 70 75 80

Gln Leu Val Glu Glu Leu Leu Lys Ile Ile Cys Ala Phe Gln Leu Asp  
85 90 95

Thr Gly Leu Glu Tyr Ala Asn Ser Tyr Asn Phe Ala Lys Lys Glu Asn  
100 105 110

Asn Ser Pro Glu His Leu Lys Asp Glu Val Ser Ile Ile Gln Ser Met  
115 120 125

Gly Tyr Arg Asn Arg Ala Lys Arg Leu Leu Gln Ser Glu Pro Glu Asn  
130 135 140

Pro Ser Leu Gln Glu Thr Ser Leu Ser Val Gln Leu Ser Asn Leu Gly  
145 150 155 160

Thr Val Arg Thr Leu Arg Thr Lys Gln Arg Ile Gln Pro Gln Lys Thr  
165 170 175

Ser Val Tyr Ile Glu Leu Gly Ser Asp Ser Ser Glu Asp Thr Val Asn  
180 185 190



Lys Ala Thr Tyr Cys Ser Val Gly Asp Gln Glu Leu Leu Gln Ile Thr  
 195 200 205  
 Pro Gln Gly Thr Arg Asp Glu Ile Ser Leu Asp Ser Ala Lys Lys Ala  
 210 215 220  
 Ala Cys Glu Phe Ser Glu Thr Asp Val Thr Asn Thr Glu His His Gln  
 225 230 235 240  
 Pro Ser Asn Asn Asp Leu Asn Thr Thr Glu Lys Arg Ala Ala Glu Arg  
 245 250 255  
 His Pro Glu Lys Tyr Gln Gly Ser Ser Val Ser Asn Leu His Val Glu  
 260 265 270  
 Pro Cys Gly Thr Asn Thr His Ala Ser Ser Leu Gln His Glu Asn Ser  
 275 280 285  
 Ser Leu Leu Leu Thr Lys Asp Arg Met Asn Val Glu Lys Ala Glu Phe  
 290 295 300  
 Cys Asn Lys Ser Lys Gln Pro Gly Leu Ala Arg Ser Gln His Asn Arg  
 305 310 315 320  
 Trp Ala Gly Ser Lys Glu Thr Cys Asn Asp Arg Arg Thr Pro Ser Thr  
 325 330 335  
 Glu Lys Lys Val Asp Leu Asn Ala Asp Pro Leu Cys Glu Arg Lys Glu  
 340 345 350  
 Trp Asn Lys Gln Lys Leu Pro Cys Ser Glu Asn Pro Arg Asp Thr Glu  
 355 360 365  
 Asp Val Pro Trp Ile Thr Leu Asn Ser Ser Ile Gln Lys Val Asn Glu  
 370 375 380  
 Trp Phe Ser Arg Ser Asp Glu Leu Leu Gly Ser Asp Asp Ser His Asp  
 385 390 395 400  
 Gly Glu Ser Glu Ser Asn Ala Lys Val Ala Asp Val Leu Asp Val Leu

405	410	415
Asn Glu Val Asp Glu Tyr Ser Gly Ser Ser Glu Lys Ile Asp Leu Leu 420	425	430
Ala Ser Asp Pro His Glu Ala Leu Ile Cys Lys Ser Glu Arg Val His 435	440	445
Ser Lys Ser Val Glu Ser Asn Ile Glu Asp Lys Ile Phe Gly Lys Thr 450	455	460
Tyr Arg Lys Lys Ala Ser Leu Pro Asn Leu Ser His Val Thr Glu Asn 465	470	475
		480
Leu Ile Ile Gly Ala Phe Val Thr Glu Pro Gln Ile Ile Gln Glu Arg 485	490	495
Pro Leu Thr Asn Lys Leu Lys Arg Lys Arg Arg Pro Thr Ser Gly Leu 500	505	510
His Pro Glu Asp Phe Ile Lys Lys Ala Asp Leu Ala Val Gln Lys Thr 515	520	525
Pro Glu Met Ile Asn Gln Gly Thr Asn Gln Thr Glu Gln Asn Gly Gln 530	535	540
Val Met Asn Ile Thr Asn Ser Gly His Glu Asn Lys Thr Lys Gly Asp 545	550	555
		560
Ser Ile Gln Asn Glu Lys Asn Pro Asn Pro Ile Glu Ser Leu Glu Lys 565	570	575
Glu Ser Ala Phe Lys Thr Lys Ala Glu Pro Ile Ser Ser Ser Ile Ser 580	585	590
Asn Met Glu Leu Glu Leu Asn Ile His Asn Ser Lys Ala Pro Lys Lys 595	600	605
Asn Arg Leu Arg Arg Lys Ser Ser Thr Arg His Ile His Ala Leu Glu 610	615	620

Leu Val Val Ser Arg Asn Leu Ser Pro Pro Asn Cys Thr Glu Leu Gln  
 625 630 635 640  
 Ile Asp Ser Cys Ser Ser Ser Glu Glu Ile Lys Lys Lys Lys Tyr Asn  
 645 650 655  
 Gln Met Pro Val Arg His Ser Arg Asn Leu Gln Leu Met Glu Gly Lys  
 660 665 670  
 Glu Pro Ala Thr Gly Ala Lys Lys Ser Asn Lys Pro Asn Glu Gln Thr  
 675 680 685  
 Ser Lys Arg His Asp Ser Asp Thr Phe Pro Glu Leu Lys Leu Thr Asn  
 690 695 700  
 Ala Pro Gly Ser Phe Thr Lys Cys Ser Asn Thr Ser Glu Leu Lys Glu  
 705 710 715 720  
 Phe Val Asn Pro Ser Leu Pro Arg Glu Glu Lys Glu Glu Lys Leu Glu  
 725 730 735  
 Thr Val Lys Val Ser Asn Asn Ala Glu Asp Pro Lys Asp Leu Met Leu  
 740 745 750  
 Ser Gly Glu Arg Val Leu Gln Thr Glu Arg Ser Val Glu Ser Ser Ser  
 755 760 765  
 Ile Ser Leu Val Pro Gly Thr Asp Tyr Gly Thr Gln Glu Ser Ile Ser  
 770 775 780  
 Leu Leu Glu Val Ser Thr Leu Gly Lys Ala Lys Thr Glu Pro Asn Lys  
 785 790 795 800  
 Cys Val Ser Gln Cys Ala Ala Phe Glu Asn Pro Lys Gly Leu Ile His  
 805 810 815  
 Gly Cys Ser Lys Asp Asn Arg Asn Asp Thr Glu Gly Phe Lys Tyr Pro  
 820 825 830  
 Leu Gly His Glu Val Asn His Ser Arg Glu Thr Ser Ile Glu Met Glu

835                      840                      845  
 Glu Ser Glu Leu Asp Ala Gln Tyr Leu Gln Asn Thr Phe Lys Val Ser  
 850                      855                      860  
 Lys Arg Gln Ser Phe Ala Leu Phe Ser Asn Pro Gly Asn Ala Glu Glu  
 865                      870                      875                      880  
 Glu Cys Ala Thr Phe Ser Ala His Ser Gly Ser Leu Lys Lys Gln Ser  
 885                      890                      895  
 Pro Lys Val Thr Phe Glu Cys Glu Gln Lys Glu Glu Asn Gln Gly Lys  
 900                      905                      910  
 Asn Glu Ser Asn Ile Lys Pro Val Gln Thr Val Asn Ile Thr Ala Gly  
 915                      920                      925  
 Phe Pro Val Val Gly Gln Lys Asp Lys Pro Val Asp Asn Ala Lys Cys  
 930                      935                      940  
 Ser Ile Lys Gly Gly Ser Arg Phe Cys Leu Ser Ser Gln Phe Arg Gly  
 945                      950                      955                      960  
 Asn Glu Thr Gly Leu Ile Thr Pro Asn Lys His Gly Leu Leu Gln Asn  
 965                      970                      975  
 Pro Tyr Arg Ile Pro Pro Leu Phe Pro Ile Lys Ser Phe Val Lys Thr  
 980                      985                      990  
 Lys Cys Lys Lys Asn Leu Leu Glu Glu Asn Phe Glu Glu His Ser Met  
 995                      1000                      1005  
 Ser Pro Glu Arg Glu Met Gly Asn Glu Asn Ile Pro Ser Thr Val Ser  
 1010                      1015                      1020  
 Thr Ile Ser Arg Asn Asn Ile Arg Glu Asn Val Phe Lys Gly Ala Ser  
 1025                      1030                      1035                      1040  
 Ser Ser Asn Ile Asn Glu Val Gly Ser Ser Thr Asn Glu Val Gly Ser  
 1045                      1050                      1055

Ser Ile Asn Glu Ile Gly Ser Ser Asp Glu Asn Ile Gln Ala Glu Leu  
 1060 1065 1070  
 Gly Arg Asn Arg Gly Pro Lys Leu Asn Ala Met Leu Arg Leu Gly Val  
 1075 1080 1085  
 Leu Gln Pro Glu Val Tyr Lys Gln Ser Leu Pro Gly Ser Asn Cys Lys  
 1090 1095 1100  
 His Pro Glu Ile Lys Lys Gln Glu Tyr Glu Glu Val Val Gln Thr Val  
 1105 1110 1115 1120  
 Asn Thr Asp Phe Ser Pro Tyr Leu Ile Ser Asp Asn Leu Glu Gln Pro  
 1125 1130 1135  
 Met Gly Ser Ser His Ala Ser Gln Val Cys Ser Glu Thr Pro Asp Asp  
 1140 1145 1150  
 Leu Leu Asp Asp Gly Glu Ile Lys Glu Asp Thr Ser Phe Ala Glu Asn  
 1155 1160 1165  
 Asp Ile Lys Glu Ser Ser Ala Val Phe Ser Lys Ser Val Gln Arg Gly  
 1170 1175 1180  
 Glu Leu Ser Arg Ser Pro Ser Pro Phe Thr His Thr His Leu Ala Gln  
 1185 1190 1195 1200  
 Gly Tyr Arg Arg Gly Ala Lys Lys Leu Glu Ser Ser Glu Glu Asn Leu  
 1205 1210 1215  
 Ser Ser Glu Asp Glu Glu Leu Pro Cys Phe Gln His Leu Leu Phe Gly  
 1220 1225 1230  
 Lys Val Asn Asn Ile Pro Ser Gln Ser Thr Arg His Ser Thr Val Ala  
 1235 1240 1245  
 Thr Glu Cys Leu Ser Lys Asn Thr Glu Glu Asn Leu Leu Ser Leu Lys  
 1250 1255 1260  
 Asn Ser Leu Asn Asp Cys Ser Asn Gln Val Ile Leu Ala Lys Ala Ser  
 1265 1270 1275 1280

Gln Glu His His Leu Ser Glu Glu Thr Lys Cys Ser Ala Ser Leu Phe  
 1285 1290 1295  
 Ser Ser Gln Cys Ser Glu Leu Glu Asp Leu Thr Ala Asn Thr Asn Thr  
 1300 1305 1310  
 Gln Asp Pro Phe Leu Ile Gly Ser Ser Lys Gln Met Arg His Gln Ser  
 1315 1320 1325  
 Glu Ser Gln Gly Val Gly Leu Ser Asp Lys Glu Leu Val Ser Asp Asp  
 1330 1335 1340  
 Glu Glu Arg Gly Thr Gly Leu Glu Glu Asn Asn Gln Glu Glu Gln Ser  
 1345 1350 1355 1360  
 Met Asp Ser Asn Leu Gly Glu Ala Ala Ser Gly Cys Glu Ser Glu Thr  
 1365 1370 1375  
 Ser Val Ser Glu Asp Cys Ser Gly Leu Ser Ser Gln Ser Asp Ile Leu  
 1380 1385 1390  
 Thr Thr Gln Gln Arg Asp Thr Met Gln His Asn Leu Ile Lys Leu Gln  
 1395 1400 1405  
 Gln Glu Met Ala Glu Leu Glu Ala Val Leu Glu Gln His Gly Ser Gln  
 1410 1415 1420  
 Pro Ser Asn Ser Tyr Pro Ser Ile Ile Ser Asp Ser Ser Ala Leu Glu  
 1425 1430 1435 1440  
 Asp Leu Arg Asn Pro Glu Gln Ser Thr Ser Glu Lys Ala Val Leu Thr  
 1445 1450 1455  
 Ser Gln Lys Ser Ser Glu Tyr Pro Ile Ser Gln Asn Pro Glu Gly Leu  
 1460 1465 1470  
 Ser Ala Asp Lys Phe Glu Val Ser Ala Asp Ser Ser Thr Ser Lys Asn  
 1475 1480 1485

Lys Glu Pro Gly Val Glu Arg Ser Ser Pro Ser Lys Cys Pro Ser Leu  
 1490. 1495 1500  
 Asp Asp Arg Trp Tyr Met His Ser Cys Ser Gly Ser Leu Gln Asn Arg  
 1505 1510 1515 1520  
 Asn Tyr Pro Ser Gln Glu Glu Leu Ile Lys Val Val Asp Val Glu Glu  
 1525 1530 1535  
 Gln Gln Leu Glu Glu Ser Gly Pro His Asp Leu Thr Glu Thr Ser Tyr  
 1540 1545 1550  
 Leu Pro Arg Gln Asp Leu Glu Gly Thr Pro Tyr Leu Glu Ser Gly Ile  
 1555 1560 1565  
 Ser Leu Phe Ser Asp Asp Pro Glu Ser Asp Pro Ser Glu Asp Arg Ala  
 1570 1575 1580  
 Pro Glu Ser Ala Arg Val Gly Asn Ile Pro Ser Ser Thr Ser Ala Leu  
 1585 1590 1595 1600  
 Lys Val Pro Gln Leu Lys Val Ala Glu Ser Ala Gln Gly Pro Ala Ala  
 1605 1610 1615  
 Ala His Thr Thr Asp Thr Ala Gly Tyr Asn Ala Met Glu Glu Ser Val  
 1620 1625 1630  
 Ser Arg Glu Lys Pro Glu Leu Thr Ala Ser Thr Glu Arg Val Asn Lys  
 1635 1640 1645  
 Arg Met Ser Met Val Val Ser Gly Leu Thr Pro Glu Glu Phe Met Leu  
 1650 1655 1660  
 Val Tyr Lys Phe Ala Arg Lys His His Ile Thr Leu Thr Asn Leu Ile  
 1665 1670 1675 1680  
 Thr Glu Glu Thr Thr His Val Val Met Lys Thr Asp Ala Glu Phe Val  
 1685 1690 1695  
 Cys Glu Arg Thr Leu Lys Tyr Phe Leu Gly Ile Ala Gly Gly Lys Trp  
 1700 1705 1710

Val Val Ser Tyr Phe Trp Val Thr Gln Ser Ile Lys Glu Arg Lys Met  
 1715 1720 1725  
 Leu Asn Glu His Asp Phe Glu Val Arg Gly Asp Val Val Asn Gly Arg  
 1730 1735 1740  
 Asn His Gln Gly Pro Lys Arg Ala Arg Glu Ser Gln Asp Arg Lys Ile  
 1745 1750 1755 1760  
 Phe Arg Gly Leu Glu Ile Cys Cys Tyr Gly Pro Phe Thr Asn Met Pro  
 1765 1770 1775  
 Thr Asp Gln Leu Glu Trp Met Val Gln Leu Cys Gly Ala Ser Val Val  
 1780 1785 1790  
 Lys Glu Leu Ser Ser Phe Thr Leu Gly Thr Gly Val His Pro Ile Val  
 1795 1800 1805  
 Val Val Gln Pro Asp Ala Trp Thr Glu Asp Asn Gly Phe His Ala Ile  
 1810 1815 1820  
 Gly Gln Met Cys Glu Ala Pro Val Val Thr Arg Glu Trp Val Leu Asp  
 1825 1830 1835 1840  
 Ser Val Ala Leu Tyr Gln Cys Gln Glu Leu Asp Thr Tyr Leu Ile Pro  
 1845 1850 1855  
 Gln Ile Pro His Ser His Tyr  
 1860

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(B) STRAIN: BRCA1

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: 17

(B) MAP POSITION: 17q21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGCTCGCTGA	GACTTCCTGG	ACCCCGCACC	AGGCTGTGGG	GTTTCTCAGA	TAAGTGGGCC	60
CCTGCGCTCA	GGAGGCCTTC	ACCCTCTGCT	CTGGGTAAAG	TTCATTGGAA	CAGAAAGAAA	120
TGGATTTATC	TGCTCTTCGC	GTTGAAGAAG	TACAAAATGT	CATTAATGCT	ATGCAGAAAA	180
TCTTAGAGTG	TCCCATCTGT	CTGGAGTTGA	TCAAGGAACC	TGTCTCCACA	AAGTGTGACC	240
ACATATTTTG	CAAATTTTGC	ATGCTGAAAC	TTCTCAACCA	GAAGAAAGGG	CCTTCACAGT	300
GTCCTTTATG	TAAGAATGAT	ATAACCAAAA	GGAGCCTACA	AGAAAGTACG	AGATTTAGTC	360
AACTTGTTGA	AGAGCTATTG	AAAATCATT	GTGCTTTTCA	GCTTGACACA	GGTTTGGAGT	420
ATGCAAACAG	CTATAATTTT	GCAAAAAAGG	AAAATAACTC	TCCTGAACAT	CTAAAAGATG	480
AAGTTTCTAT	CATCCAAAGT	ATGGGCTACA	GAAACCGTGC	CAAAGACTT	CTACAGAGTG	540
AACCCGAAAA	TCCTTCCTTG	CAGGAAACCA	GTCTCAGTGT	CCAACTCTCT	AACCTTGGA	600
CTGTGAGAAC	TCTGAGGACA	AAGCAGCGGA	TACAACCTCA	AAAGACGTCT	GTCTACATTG	660
AATTGGGATC	TGATTCTTCT	GAAGATACCG	TTAATAAGGC	AACTTATTGC	AGTGTGGGAG	720
ATCAAGAATT	GTTACAAATC	ACCCCTCAAG	GAACCAGGGA	TGAAATCAGT	TTGGATTCTG	780

CAAAAAAGGC	TGCTTGTGAA	TTTTCTGAGA	CGGATGTAAC	AAATACTGAA	CATCATCAAC	840
CCAGTAATAA	TGATTTGAAC	ACCACTGAGA	AGCGTGCAGC	TGAGAGGCAT	CCAGAAAAGT	900
ATCAGGGTAG	TTCTGTTTCA	AACTTGCATG	TGGAGCCATG	TGGCACAAAT	ACTCATGCCA	960
GCTCATTACA	GCATGAGAAC	AGCAGTTTAT	TACTCACTAA	AGACAGAATG	AATGTAGAAA	1020
AGGCTGAATT	CTGTAATAAA	AGCAAACAGC	CTGGCTTAGC	AAGGAGCCAA	CATAACAGAT	1080
GGGCTGGAAG	TAAGGAAACA	TGTAATGATA	GCGGACTCC	CAGCACAGAA	AAAAAGGTAG	1140
ATCTGAATGC	TGATCCCCTG	TGTGAGAGAA	AAGAATGGAA	TAAGCAGAAA	CTGCCATGCT	1200
CAGAGAATCC	TAGAGATACT	GAAGATGTTT	CTTGGATAAC	ACTAAATAGC	AGCATTCAGA	1260
AAGTTAATGA	GTGGTTTTCC	AGAAGTGATG	AACTGTTAGG	TTCTGATGAC	TCACATGATG	1320
GGGAGTCTGA	ATCAAATGCC	AAAGTAGCTG	ATGTATTGGA	CGTTCTAAAT	GAGGTAGATG	1380
AATATTCTGG	TTCTTCAGAG	AAAATAGACT	TACTGGCCAG	TGATCCTCAT	GAGGCTTTAA	1440
TATGTAAAAG	TGAAAGAGTT	CACTCCAAAT	CAGTAGAGAG	TAATATTGAA	GACAAAATAT	1500
TTGGGAAAAC	CTATCGGAAG	AAGGCAAGCC	TCCCCAACTT	AAGCCATGTA	ACTGAAAATC	1560
TAATTATAGG	AGCATTTGTT	ACTGAGCCAC	AGATAATACA	AGAGCGTCCC	CTCACAAATA	1620
AATTAAAGCG	TAAAAGGAGA	CCTACATCAG	GCCTTCATCC	TGAGGATTTT	ATCAAGAAAG	1680
CAGATTTGGC	AGTTCAAAAAG	ACTCCTGAAA	TGATAAATCA	GGGAACTAAC	CAAACGGAGC	1740
AGAATGGTCA	AGTGATGAAT	ATTACTAATA	GTGGTCATGA	GAATAAAACA	AAAGGTGATT	1800
CTATTCAGAA	TGAGAAAAAT	CCTAACCCAA	TAGAATCACT	CGAAAAAGAA	TCTGCTTTCA	1860
AAACGAAAGC	TGAACCTATA	AGCAGCAGTA	TAAGCAATAT	GGAACTCGAA	TTAAATATCC	1920
ACAATTCAAA	AGCACCTAAA	AAGAATAGGC	TGAGGAGGAA	GTCTTCTACC	AGGCATATTC	1980

ATGCGCTTGA	ACTAGTAGTC	AGTAGAAATC	TAAGCCCACC	TAATTGTACT	GAATTGCAAA	201
TTGATAGTTG	TTCTAGCAGT	GAAGAGATAA	AGAAAAAAAA	GTACAACCAA	ATGCCAGTCA	210
GGCACAGCAG	AAACCTACAA	CTCATGGAAG	GTAAAGAACC	TGCAACTGGA	GCCAAGAAGA	216
GTAACAAGCC	AAATGAACAG	ACAAGTAAAA	GACATGACAG	CGATACTTTC	CCAGAGCTGA	222
AGTTAACAAA	TGCACCTGGT	TCTTTTACTA	AGTGTTCAAA	TACCAGTGAA	CTTAAAGAAT	228
TTGTCAATCC	TAGCCTTCCA	AGAGAAGAAA	AAGAAGAGAA	ACTAGAAACA	GTTAAAGTGT	234
CTAATAATGC	TGAAGACCCC	AAAGATCTCA	TGTTAAGTGG	AGAAAGGGTT	TTGCAAACCTG	240
AAAGATCTGT	AGAGAGTAGC	AGTATTTTCAT	TGGTACCTGG	TACTGATTAT	GGCACTCAGG	246
AAAGTATCTC	GTTACTGGAA	GTTAGCACTC	TAGGGAAGGC	AAAAACAGAA	CCAAATAAAT	252
GTGTGAGTCA	GTGTGCAGCA	TTTGAAAACC	CCAAGGGACT	AATTCATGGT	TGTTCCAAAG	258
ATAATAGAAA	TGACACAGAA	GGCTTTAAGT	ATCCATTGGG	ACATGAAGTT	AACCACAGTC	264
GGGAAACAAG	CATAGAAATG	GAAGAAAGTG	AACTTGATGC	TCAGTATTTG	CAGAATACAT	270
TCAAGGTTTC	AAAGCGCCAG	TCATTTGCTC	TGTTTTCAAA	TCCAGGAAAT	GCAGAAGAGG	276
AATGTGCAAC	ATTCTCTGCC	CACTCTGGGT	CCTTAAAGAA	ACAAAGTCCA	AAAGTCACTT	282
TTGAATGTGA	ACAAAAGGAA	GAAAATCAAG	GAAAGAATGA	GTCTAATATC	AAGCCTGTAC	288
AGACAGTTAA	TATCACTGCA	GGCTTTCCTG	TGGTTGGTCA	GAAAGATAAG	CCAGTTGATA	294
ATGCCAAATG	TAGTATCAAA	GGAGGCTCTA	GGTTTTGTCT	ATCATCTCAG	TTCAGAGGCA	300
ACGAAACTGG	ACTCATTACT	CCAAATAAAC	ATGGACTTTT	ACAAAACCCA	TATCGTATAC	306
CACCACTTTT	TCCCATCAAG	TCATTTGTTA	AACTAAATG	TAAGAAAAAT	CTGCTAGAGG	312
AAAACTTTGA	GGAACATTCA	ATGTCACCTG	AAAGAGAAAT	GGGAAATGAG	AACATTCCAA	318

GTACAGTGAG	CACAATTAGC	CGTAATAACA	TTAGAGAAAA	TGTTTTTAAA	GAAGCCAGCT	324
CAAGCAATAT	TAATGAAGTA	GGTTCAGTA	CTAATGAAGT	GGGCTCCAGT	ATTAATGAAA	330
TAGGTTCCAG	TGATGAAAAC	ATTCAAGCAG	AACTAGGTAG	AAACAGAGGG	CCAAAATTGA	336
ATGCTATGCT	TAGATTAGGG	GTTTTGCAAC	CTGAGGTCTA	TAAACAAAGT	CTTCCTGGAA	342
GTAATTGTAA	GCATCCTGAA	ATAAAAAAGC	AAGAATATGA	AGAAGTAGTT	CAGACTGTTA	348
ATACAGATTT	CTCTCCATAT	CTGATTTTCT	ATAACTTAGA	ACAGCCTATG	GGAAGTAGTC	354
ATGCATCTCA	GGTTTGTTCT	GAGACACCTG	ATGACCTGTT	AGATGATGGT	GAAATAAAGG	360
AAGATACTAG	TTTGCTGAA	AATGACATTA	AGGAAAGTTC	TGCTGTTTTT	AGCAAAAGCG	366
TCCAGAAAGG	AGAGCTTAGC	AGGAGTCCTA	GCCCTTTCAC	CCATACACAT	TTGGCTCAGG	372
GTTACCGAAG	AGGGGCCAAG	AAATTAGAGT	CCTCAGAAGA	GAACCTATCT	AGTGAGGATG	378
AAGAGCTTCC	CTGCTTCCAA	CACTTGTTAT	TTGGTAAAGT	AAACAATATA	CCTTCTCAGT	384
CTACTAGGCA	TAGCACCGTT	GCTACCGAGT	GTCTGTCTAA	GAACACAGAG	GAGAATTTAT	390
TATCATTGAA	GAATAGCTTA	AATGACTGCA	GTAACCAGGT	AATATTGGCA	AAGGCATCTC	396
AGGAACATCA	CCTTAGTGAG	GAAACAAAAT	GTTCTGCTAG	CTTGTTTTCT	TCACAGTGCA	402
GTGAATTGGA	AGACTTGACT	GCAAATACAA	ACACCCAGGA	TCCTTTCTTG	ATTGGTTCTT	408
CCAAACAAAT	GAGGCATCAG	TCTGAAAGCC	AGGGAGTTGG	TCTGAGTGAC	AAGGAATTGG	414
TTTCAGATGA	TGAAGAAAGA	GGAACGGGCT	TGGAAGAAAA	TAATCAAGAA	GAGCAAAGCA	420
TGGATTCAAA	CTTAGGTGAA	GCAGCATCTG	GGTGTGAGAG	TGAAACAAGC	GTCTCTGAAG	426
ACTGCTCAGG	GCTATCCTCT	CAGAGTGACA	TTTTAACCAC	TCAGCAGAGG	GATACCATGC	432
AACATAACCT	GATAAAGCTC	CAGCAGGAAA	TGGCTGAACT	AGAAGCTGTG	TTAGAACAGC	438

ATGGGAGCCA	GCCTTCTAAC	AGCTACCCTT	CCATCATAAG	TGACTCTTCT	GCCCTTGAGG	44
ACCTGCGAAA	TCCAGAACAA	AGCACATCAG	AAAAAGCAGT	ATTAAGTTCA	CAGAAAAGTA	450
GTGAATACCC	TATAAGCCAG	AATCCAGAAG	GCCTTTCTGC	TGACAAGTTT	GAGGTGTCTG	456
CAGATAGTTC	TACCAGTAAA	AATAAAGAAC	CAGGAGTGGA	AAGGTCATCC	CCTTCTAAAT	462
GCCCATCATT	AGATGATAGG	TGGTACATGC	ACAGTTGCTC	TGGGAGTCTT	CAGAATAGAA	468
ACTACCCATC	TCAAGAGGAG	CTCATTAAGG	TTGTTGATGT	GGAGGAGCAA	CAGCTGGAAG	474
AGTCTGGGCC	ACACGATTTG	ACGGAAACAT	CTTACTTGCC	AAGGCAAGAT	CTAGAGGGAA	480
CCCCTTACCT	GGAATCTGGA	ATCAGCCTCT	TCTCTGATGA	CCCTGAATCT	GATCCTTCTG	486
AAGACAGAGC	CCCAGAGTCA	GCTCGTGTG	GCAACATACC	ATCTTCAACC	TCTGCATTGA	492
AAGTTCCCCA	ATTGAAAGTT	GCAGAATCTG	CCCAGAGTCC	AGCTGCTGCT	CATACTACTG	4980
ATACTGCTGG	GTATAATGCA	ATGGAAGAAA	GTGTGAGCAG	GGAGAAGCCA	GAATTGACAG	5040
CTTCAACAGA	AAGGGTCAAC	AAAAGAATGT	CCATGGTGGT	GTCTGGCCTG	ACCCCAGAAG	5100
AATTTATGCT	CGTGTTACAAG	TTTGCCAGAA	AACACCACAT	CACTTTAACT	AATCTAATTA	5160
CTGAAGAGAC	TACTCATGTT	GTTATGAAAA	CAGATGCTGA	GTTTGTGTGT	GAACGGACAC	5220
TGAAATATTT	TCTAGGAATT	GCGGGAGGAA	AATGGGTAGT	TAGCTATTTT	TGGGTGACCC	5280
AGTCTATTAA	AGAAAGAAAA	ATGCTGAATG	AGCATGATTT	TGAAGTCAGA	GGAGATGTGG	5340
TCAATGGAAG	AAACCACCAA	GGTCCAAAGC	GAGCAAGAGA	ATCCCAGGAC	AGAAAGATCT	5400
TCAGGGGGCT	AGAAATCTGT	TGCTATGGGC	CCTTCACCAA	CATGCCCCACA	GATCAACTGG	5460
AATGGATGGT	ACAGCTGTGT	GGTGCTTCTG	TGGTGAAGGA	GCTTTCATCA	TTCACCCTTG	5520
GCACAGGTGT	CCACCCAATT	GTGGTTGTGC	AGCCAGATGC	CTGGACAGAG	GACAATGGCT	5580

TCCATGCAAT TGGGCAGATG TGTGAGGCAC CTGTGGTGAC CCGAGAGTGG GTGTTGGACA 5640  
 GTGTAGCACT CTACCACTGC CAGGAGCTGG ACACCTACCT GATACCCCAG ATCCCCCACA 5700  
 GCCACTACTG A 5711

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1863 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (B) STRAIN: BRCA1

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: 17
- (B) MAP POSITION: 17q21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asp	Leu	Ser	Ala	Leu	Arg	Val	Glu	Glu	Val	Gln	Asn	Val	Ile	Asn	1	5	10	15
Ala	Met	Gln	Lys	Ile	Leu	Glu	Cys	Pro	Ile	Cys	Leu	Glu	Leu	Ile	Lys	20	25	30	
Glu	Pro	Val	Ser	Thr	Lys	Cys	Asp	His	Ile	Phe	Cys	Lys	Phe	Cys	Met	35	40	45	
Leu	Lys	Leu	Leu	Asn	Gln	Lys	Lys	Gly	Pro	Ser	Gln	Cys	Pro	Leu	Cys	50	55	60	

Lys Asn Asp Ile Thr Lys Arg Ser Leu Gln Glu Ser Thr Arg Phe Ser  
 65 70 75 80  
 Gln Leu Val Glu Glu Leu Leu Lys Ile Ile Cys Ala Phe Gln Leu Asp  
 85 90 95  
 Thr Gly Leu Glu Tyr Ala Asn Ser Tyr Asn Phe Ala Lys Lys Glu Asn  
 100 105 110  
 Asn Ser Pro Glu His Leu Lys Asp Glu Val Ser Ile Ile Gln Ser Met  
 115 120 125  
 Gly Tyr Arg Asn Arg Ala Lys Arg Leu Leu Gln Ser Glu Pro Glu Asn  
 130 135 140  
 Pro Ser Leu Gln Glu Thr Ser Leu Ser Val Gln Leu Ser Asn Leu Gly  
 145 150 155 160  
 Thr Val Arg Thr Leu Arg Thr Lys Gln Arg Ile Gln Pro Gln Lys Thr  
 165 170 175  
 Ser Val Tyr Ile Glu Leu Gly Ser Asp Ser Ser Glu Asp Thr Val Asn  
 180 185 190  
 Lys Ala Thr Tyr Cys Ser Val Gly Asp Gln Glu Leu Leu Gln Ile Thr  
 195 200 205  
 Pro Gln Gly Thr Arg Asp Glu Ile Ser Leu Asp Ser Ala Lys Lys Ala  
 210 215 220  
 Ala Cys Glu Phe Ser Glu Thr Asp Val Thr Asn Thr Glu His His Gln  
 225 230 235 240  
 Pro Ser Asn Asn Asp Leu Asn Thr Thr Glu Lys Arg Ala Ala Glu Arg  
 245 250 255  
 His Pro Glu Lys Tyr Gln Gly Ser Ser Val Ser Asn Leu His Val Glu  
 260 265 270

Pro Cys Gly Thr Asn Thr His Ala Ser Ser Leu Gln His Glu Asn Ser  
 275 280 285  
 Ser Leu Leu Leu Thr Lys Asp Arg Met Asn Val Glu Lys Ala Glu Phe  
 290 295 300  
 Cys Asn Lys Ser Lys Gln Pro Gly Leu Ala Arg Ser Gln His Asn Arg  
 305 310 315 320  
 Trp Ala Gly Ser Lys Glu Thr Cys Asn Asp Arg Arg Thr Pro Ser Thr  
 325 330 335  
 Glu Lys Lys Val Asp Leu Asn Ala Asp Pro Leu Cys Glu Arg Lys Glu  
 340 345 350  
 Trp Asn Lys Gln Lys Leu Pro Cys Ser Glu Asn Pro Arg Asp Thr Glu  
 355 360 365  
 Asp Val Pro Trp Ile Thr Leu Asn Ser Ser Ile Gln Lys Val Asn Glu  
 370 375 380  
 Trp Phe Ser Arg Ser Asp Glu Leu Leu Gly Ser Asp Asp Ser His Asp  
 385 390 395 400  
 Gly Glu Ser Glu Ser Asn Ala Lys Val Ala Asp Val Leu Asp Val Leu  
 405 410 415  
 Asn Glu Val Asp Glu Tyr Ser Gly Ser Ser Glu Lys Ile Asp Leu Leu  
 420 425 430  
 Ala Ser Asp Pro His Glu Ala Leu Ile Cys Lys Ser Glu Arg Val His  
 435 440 445  
 Ser Lys Ser Val Glu Ser Asn Ile Glu Asp Lys Ile Phe Gly Lys Thr  
 450 455 460  
 Tyr Arg Lys Lys Ala Ser Leu Pro Asn Leu Ser His Val Thr Glu Asn  
 465 470 475 480  
 Leu Ile Ile Gly Ala Phe Val Thr Glu Pro Gln Ile Ile Gln Glu Arg



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Ala Pro Gly Ser Phe Thr Lys Cys Ser Asn Thr Ser Glu Leu Lys Glu  
 705 710 715 720  
 Phe Val Asn Pro Ser Leu Pro Arg Glu Glu Lys Glu Glu Lys Leu Glu  
 725 730 735  
 Thr Val Lys Val Ser Asn Asn Ala Glu Asp Pro Lys Asp Leu Met Leu  
 740 745 750  
 Ser Gly Glu Arg Val Leu Gln Thr Glu Arg Ser Val Glu Ser Ser Ser  
 755 760 765  
 Ile Ser Leu Val Pro Gly Thr Asp Tyr Gly Thr Gln Glu Ser Ile Ser  
 770 775 780  
 Leu Leu Glu Val Ser Thr Leu Gly Lys Ala Lys Thr Glu Pro Asn Lys  
 785 790 795 800  
 Cys Val Ser Gln Cys Ala Ala Phe Glu Asn Pro Lys Gly Leu Ile His  
 805 810 815  
 Gly Cys Ser Lys Asp Asn Arg Asn Asp Thr Glu Gly Phe Lys Tyr Pro  
 820 825 830  
 Leu Gly His Glu Val Asn His Ser Arg Glu Thr Ser Ile Glu Met Glu  
 835 840 845  
 Glu Ser Glu Leu Asp Ala Gln Tyr Leu Gln Asn Thr Phe Lys Val Ser  
 850 855 860  
 Lys Arg Gln Ser Phe Ala Leu Phe Ser Asn Pro Gly Asn Ala Glu Glu  
 865 870 875 880  
 Glu Cys Ala Thr Phe Ser Ala His Ser Gly Ser Leu Lys Lys Gln Ser  
 885 890 895  
 Pro Lys Val Thr Phe Glu Cys Glu Gln Lys Glu Glu Asn Gln Gly Lys  
 900 905 910  
 Asn Glu Ser Asn Ile Lys Pro Val Gln Thr Val Asn Ile Thr Ala Gly  
 915 920 925

Phe Pro Val Val Gly Gln Lys Asp Lys Pro Val Asp Asn Ala Lys Cys  
 930 935 940

Ser Ile Lys Gly Gly Ser Arg Phe Cys Leu Ser Ser Gln Phe Arg Gly  
 945 950 955 960

Asn Glu Thr Gly Leu Ile Thr Pro Asn Lys His Gly Leu Leu Gln Asn  
 965 970 975

Pro Tyr Arg Ile Pro Pro Leu Phe Pro Ile Lys Ser Phe Val Lys Thr  
 980 985 990

Lys Cys Lys Lys Asn Leu Leu Glu Glu Asn Phe Glu Glu His Ser Met  
 995 1000 1005

Ser Pro Glu Arg Glu Met Gly Asn Glu Asn Ile Pro Ser Thr Val Ser  
 1010 1015 1020

Thr Ile Ser Arg Asn Asn Ile Arg Glu Asn Val Phe Lys Glu Ala Ser  
 1025 1030 1035 1040

Ser Ser Asn Ile Asn Glu Val Gly Ser Ser Thr Asn Glu Val Gly Ser  
 1045 1050 1055

Ser Ile Asn Glu Ile Gly Ser Ser Asp Glu Asn Ile Gln Ala Glu Leu  
 1060 1065 1070

Gly Arg Asn Arg Gly Pro Lys Leu Asn Ala Met Leu Arg Leu Gly Val  
 1075 1080 1085

Leu Gln Pro Glu Val Tyr Lys Gln Ser Leu Pro Gly Ser Asn Cys Lys  
 1090 1095 1100

His Pro Glu Ile Lys Lys Gln Glu Tyr Glu Glu Val Val Gln Thr Val  
 1105 1110 1115 1120

Asn Thr Asp Phe Ser Pro Tyr Leu Ile Ser Asp Asn Leu Glu Gln Pro  
 1125 1130 1135

Met Gly Ser Ser His Ala Ser Gln Val Cys Ser Glu Thr Pro Asp Asp  
 1140 1145 1150  
 Leu Leu Asp Asp Gly Glu Ile Lys Glu Asp Thr Ser Phe Ala Glu Asn  
 1155 1160 1165  
 Asp Ile Lys Glu Ser Ser Ala Val Phe Ser Lys Ser Val Gln Lys Gly  
 1170 1175 1180  
 Glu Leu Ser Arg Ser Pro Ser Pro Phe Thr His Thr His Leu Ala Gln  
 1185 1190 1195 1200  
 Gly Tyr Arg Arg Gly Ala Lys Lys Leu Glu Ser Ser Glu Glu Asn Leu  
 1205 1210 1215  
 Ser Ser Glu Asp Glu Glu Leu Pro Cys Phe Gln His Leu Leu Phe Gly  
 1220 1225 1230  
 Lys Val Asn Asn Ile Pro Ser Gln Ser Thr Arg His Ser Thr Val Ala  
 1235 1240 1245  
 Thr Glu Cys Leu Ser Lys Asn Thr Glu Glu Asn Leu Leu Ser Leu Lys  
 1250 1255 1260  
 Asn Ser Leu Asn Asp Cys Ser Asn Gln Val Ile Leu Ala Lys Ala Ser  
 1265 1270 1275 1280  
 Gln Glu His His Leu Ser Glu Glu Thr Lys Cys Ser Ala Ser Leu Phe  
 1285 1290 1295  
 Ser Ser Gln Cys Ser Glu Leu Glu Asp Leu Thr Ala Asn Thr Asn Thr  
 1300 1305 1310  
 Gln Asp Pro Phe Leu Ile Gly Ser Ser Lys Gln Met Arg His Gln Ser  
 1315 1320 1325  
 Glu Ser Gln Gly Val Gly Leu Ser Asp Lys Glu Leu Val Ser Asp Asp  
 1330 1335 1340  
 Glu Glu Arg Gly Thr Gly Leu Glu Glu Asn Asn Gln Glu Glu Gln Ser  
 1345 1350 1355 1360

Met Asp Ser Asn Leu Gly Glu Ala Ala Ser Gly Cys Glu Ser Glu Thr  
1365 1370 1375

Ser Val Ser Glu Asp Cys Ser Gly Leu Ser Ser Gln Ser Asp Ile Leu  
1380 1385 1390

Thr Thr Gln Gln Arg Asp Thr Met Gln His Asn Leu Ile Lys Leu Gln  
1395 1400 1405

Gln Glu Met Ala Glu Leu Glu Ala Val Leu Glu Gln His Gly Ser Gln  
1410 1415 1420

Pro Ser Asn Ser Tyr Pro Ser Ile Ile Ser Asp Ser Ser Ala Leu Glu  
1425 1430 1435 1440

Asp Leu Arg Asn Pro Glu Gln Ser Thr Ser Glu Lys Ala Val Leu Thr  
1445 1450 1455

Ser Gln Lys Ser Ser Glu Tyr Pro Ile Ser Gln Asn Pro Glu Gly Leu  
1460 1465 1470

Ser Ala Asp Lys Phe Glu Val Ser Ala Asp Ser Ser Thr Ser Lys Asn  
1475 1480 1485

Lys Glu Pro Gly Val Glu Arg Ser Ser Pro Ser Lys Cys Pro Ser Leu  
1490 1495 1500

Asp Asp Arg Trp Tyr Met His Ser Cys Ser Gly Ser Leu Gln Asn Arg  
1505 1510 1515 1520

Asn Tyr Pro Ser Gln Glu Glu Leu Ile Lys Val Val Asp Val Glu Glu  
1525 1530 1535

Gln Gln Leu Glu Glu Ser Gly Pro His Asp Leu Thr Glu Thr Ser Tyr  
1540 1545 1550

Leu Pro Arg Gln Asp Leu Glu Gly Thr Pro Tyr Leu Glu Ser Gly Ile  
1555 1560 1565

Ser Leu Phe Ser Asp Asp Pro Glu Ser Asp Pro Ser Glu Asp Arg Ala

1570                      1575                      1580  
 Pro Glu Ser Ala Arg Val Gly Asn Ile Pro Ser Ser Thr Ser Ala Leu  
 1585                      1590                      1595                      1600  
 Lys Val Pro Gln Leu Lys Val Ala Glu Ser Ala Gln Ser Pro Ala Ala  
                     1605                      1610                      1615  
 Ala His Thr Thr Asp Thr Ala Gly Tyr Asn Ala Met Glu Glu Ser Val  
                     1620                      1625                      1630  
 Ser Arg Glu Lys Pro Glu Leu Thr Ala Ser Thr Glu Arg Val Asn Lys  
                     1635                      1640                      1645  
 Arg Met Ser Met Val Val Ser Gly Leu Thr Pro Glu Glu Phe Met Leu  
                     1650                      1655                      1660  
 Val Tyr Lys Phe Ala Arg Lys His His Ile Thr Leu Thr Asn Leu Ile  
 1665                      1670                      1675                      1680  
 Thr Glu Glu Thr Thr His Val Val Met Lys Thr Asp Ala Glu Phe Val  
                     1685                      1690                      1695  
 Cys Glu Arg Thr Leu Lys Tyr Phe Leu Gly Ile Ala Gly Gly Lys Trp  
                     1700                      1705                      1710  
 Val Val Ser Tyr Phe Trp Val Thr Gln Ser Ile Lys Glu Arg Lys Met  
                     1715                      1720                      1725  
 Leu Asn Glu His Asp Phe Glu Val Arg Gly Asp Val Val Asn Gly Arg  
                     1730                      1735                      1740  
 Asn His Gln Gly Pro Lys Arg Ala Arg Glu Ser Gln Asp Arg Lys Ile  
 1745                      1750                      1755                      1760  
 Phe Arg Gly Leu Glu Ile Cys Cys Tyr Gly Pro Phe Thr Asn Met Pro  
                     1765                      1770                      1775  
 Thr Asp Gln Leu Glu Trp Met Val Gln Leu Cys Gly Ala Ser Val Val  
                     1780                      1785                      1790

Lys Glu Leu Ser Ser Phe Thr Leu Gly Thr Gly Val His Pro Ile Val  
           1795                                  1800                                  1805  
 Val Val Gln Pro Asp Ala Trp Thr Glu Asp Asn Gly Phe His Ala Ile  
           1810                                  1815                                  1820  
  
 Gly Gln Met Cys Glu Ala Pro Val Val Thr Arg Glu Trp Val Leu Asp  
 1825                                  1830                                  1835                                  1840  
  
 Ser Val Ala Leu Tyr Gln Cys Gln Glu Leu Asp Thr Tyr Leu Ile Pro  
                                   1845                                  1850                                  1855  
  
 Gln Ile Pro His Ser His Tyr  
                                   1860

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (B) STRAIN: BRCA1

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: 17
- (B) MAP POSITION: 17q21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGCTCGCTGA	GACTTCCTGG	ACCCCGCACC	AGGCTGTGGG	GTTTCTCAGA	TAAGTGGGCC	60
CCTGCGCTCA	GGAGGCCTTC	ACCCTCTGCT	CTGGGTAAAG	TTCATTGGAA	CAGAAAGAAA	120
TGGATTTATC	TGCTCTTCGC	GTTGAAGAAG	TACAAAATGT	CATTAATGCT	ATGCAGAAAA	180
TCTTAGAGTG	TCCCATCTGT	CTGGAGTTGA	TCAAGGAACC	TGTCTCCACA	AAGTGTGACC	240
ACATATTTTG	CAAATTTTGC	ATGCTGAAAC	TTCTCAACCA	GAAGAAAGGG	CCTTCACAGT	300
GTCCTTTATG	TAAGAATGAT	ATAACCAAAA	GGAGCCTACA	AGAAAGTACG	AGATTTAGTC	360
AACTTGTTGA	AGAGCTATTG	AAAATCATT	GTGCTTTTCA	GCTTGACACA	GGTTTGGAGT	420
ATGCAAACAG	CTATAATTTT	GCAAAAAAGG	AAAATAACTC	TCCTGAACAT	CTAAAAGATG	480
AAGTTTCTAT	CATCCAAAGT	ATGGGCTACA	GAAACCGTGC	CAAAAGACTT	CTACAGAGTG	540
AACCCGAAAA	TCCTTCCTTG	CAGGAAACCA	GTCTCAGTGT	CCAACCTCTCT	AACCTTGGA	600
CTGTGAGAAC	TCTGAGGACA	AAGCAGCGGA	TACAACCTCA	AAAGACGTCT	GTCTACATTG	660
AATTGGGATC	TGATTCTTCT	GAAGATACCG	TTAATAAGGC	AACTTATTGC	AGTGTGGGAG	720
ATCAAGAATT	GTTACAAATC	ACCCCTCAAG	GAACCAGGGA	TGAAATCAGT	TTGGATTCTG	780
CAAAAAAGGC	TGCTTGTGAA	TTTTCTGAGA	CGGATGTAAC	AAATACTGAA	CATCATCAAC	840
CCAGTAATAA	TGATTTGAAC	ACCACTGAGA	AGCGTGCAGC	TGAGAGGCAT	CCAGAAAAGT	900
ATCAGGGTAG	TTCTGTTTCA	AACTTGCATG	TGGAGCCATG	TGGCACAAAT	ACTCATGCCA	960
GCTCATTACA	GCATGAGAAC	AGCAGTTTAT	TACTCACTAA	AGACAGAATG	AATGTAGAAA	1020
AGGCTGAATT	CTGTAATAAA	AGCAAACAGC	CTGGCTTAGC	AAGGAGCCAA	CATAACAGAT	1080
GGGCTGGAAG	TAAGGAAACA	TGTAATGATA	GGCGGACTCC	CAGCACAGAA	AAAAAGGTAG	1140
ATCTGAATGC	TGATCCCCTG	TGTGAGAGAA	AAGAATGGAA	TAAGCAGAAA	CTGCCATGCT	1200



CAGAGAATCC	TAGAGATACT	GAAGATGTTC	CTTGGATAAC	ACTAAATAGC	AGCATTCAGA	1260
AAGTTAATGA	GTGGTTTTCC	AGAAGTGATG	AACTGTTAGG	TTCTGATGAC	TCACATGATG	1320
GGGAGTCTGA	ATCAAATGCC	AAAGTAGCTG	ATGTATTGGA	CGTTCTAAAT	GAGGTAGATG	1380
AATATTCTGG	TTCTTCAGAG	AAAATAGACT	TACTGGCCAG	TGATCCTCAT	GAGGCTTTAA	1440
TATGTAAAAG	TGAAAGAGTT	CACTCCAAAT	CAGTAGAGAG	TAATATTGAA	GACAAAATAT	1500
TTGGGAAAAC	CTATCGGAAG	AAGGCAAGCC	TCCCCAACTT	AAGCCATGTA	ACTGAAAATC	1560
TAATTATAGG	AGCATTTGTT	ACTGAGCCAC	AGATAATACA	AGAGCGTCCC	CTCACAAATA	1620
AATTAAAGCG	TAAAAGGAGA	CCTACATCAG	GCCTTCATCC	TGAGGATTTT	ATCAAGAAAG	1680
CAGATTTGGC	AGTTCAAAAG	ACTCCTGAAA	TGATAAATCA	GGGAAC TAAC	CAAACGGAGC	1740
AGAATGGTCA	AGTGATGAAT	ATTACTAATA	GTGGTCATGA	GAATAAAACA	AAAGGTGATT	1800
CTATTCAGAA	TGAGAAAAAT	CCTAACCCAA	TAGAATCACT	CGAAAAAGAA	TCTGCTTTCA	1860
AAACGAAAGC	TGAACCTATA	AGCAGCAGTA	TAAGCAATAT	GGAAC TCGAA	TTAAATATCC	1920
ACAATTCAAA	AGCACCTAAA	AAGAATAGGC	TGAGGAGGAA	GTCTTCTACC	AGGCATATTC	1980
ATGCGCTTGA	ACTAGTAGTC	AGTAGAAATC	TAAGCCCACC	TAATTGTACT	GAATTGCAAA	2040
TTGATAGTTG	TTCTAGCAGT	GAAGAGATAA	AGAAAAA AAA	GTACAACCAA	ATGCCAGTCA	2100
GGCACAGCAG	AAACCTACAA	CTCATGGAAG	GTAAAGAACC	TGCAACTGGA	GCCAAGAAGA	2160
GTAACAAGCC	AAATGAACAG	ACAAGTAAAA	GACATGACAG	TGATACTTTC	CCAGAGCTGA	2220
AGTTAACAAA	TGCACCTGGT	TCTTTTACTA	AGTGTTCAAA	TACCAGTGAA	CTTAAAGAAT	2280
TTGTCAATCC	TAGCCTTCCA	AGAGAAGAAA	AAGAAGAGAA	ACTAGAAACA	GTAAAGTGT	2340
CTAATAATGC	TGAAGACCCC	AAAGATCTCA	TGTTAAGTGG	AGAAAGGGTT	TTGCAA ACTG	2400

AAAGATCTGT AGAGAGTAGC AGTATTTTAC TGGTACCTGG TACTGATTAT GGCACCTCAGG	2460
AAAGTATCTC GTTACTGGAA GTTAGCACTC TAGGGAAGGC AAAACAGAA CCAAATAAAT	2520
GTGTGAGTCA GTGTGCAGCA TTTGAAAACC CCAAGGGACT AATTCATGGT TGTTCCAAAG	2580
ATAATAGAAA TGACACAGAA GGCTTTAAGT ATCCATTGGG ACATGAAGTT AACCACAGTC	2640
GGGAAACAAG CATAGAAATG GAAGAAAGTG AACTTGATGC TCAGTATTTG CAGAATACAT	2700
TCAAGGTTTC AAAGCGCCAG TCATTTGCTC TGTTTTCAA TCCAGGAAAT GCAGAAGAGG	2760
AATGTGCAAC ATTCTCTGCC CACTCTGGGT CCTTAAAGAA ACAAAGTCCA AAAGTCACTT	2820
TTGAATGTGA ACAAAGGAA GAAAATCAAG GAAAGAATGA GTCTAATATC AAGCCTGTAC	2880
AGACAGTTAA TATCACTGCA GGCTTTCCTG TGGTTGGTCA GAAAGATAAG CCAGTTGATA	2940
ATGCCAAATG TAGTATCAAA GGAGGCTCTA GGTTTTGTCT ATCATCTCAG TTCAGAGGCA	3000
ACGAAACTGG ACTCATTACT CCAAATAAAC ATGGACTTTT ACAAACCCA TATCGTATAC	3060
CACCACTTTT TCCCATCAAG TCATTTGTTA AACTAAATG TAAGAAAAAT CTGCTAGAGG	3120
AAACTTTTGA GGAACATTCA ATGTCACCTG AAAGAGAAAT GGGAAATGAG AACATTCCAA	3180
GTACAGTGAG CACAATTAGC CGTAATAACA TTAGAGAAAA TGTTTTTAAA GGAGCCAGCT	3240
CAAGCAATAT TAATGAAGTA GGTTCCAGTA CTAATGAAGT GGGCTCCAGT ATTAATGAAA	3300
TAGGTTCCAG TGATGAAAAC ATTCAAGCAG AACTAGGTAG AAACAGAGGG CCAAATTTGA	3360
ATGCTATGCT TAGATTAGGG GTTTTGCAAC CTGAGGTCTA TAAACAAAGT CTTCTTGAA	3420
GTAATTGTAA GCATCCTGAA ATAAAAAGC AAGAATATGA AGAAGTAGTT CAGACTGTTA	3480
ATACAGATTT CTCTCCATAT CTGATTTTCTG ATAACCTAGA ACAGCCTATG GGAAGTAGTC	3540
ATGCATCTCA GGTTTGTTCT GAGACACCTG ATGACCTGTT AGATGATGGT GAAATAAAGG	3600

AAGATACTAG	TTTTGCTGAA	AATGACATTA	AGGAAAGTTC	TGCTGTTTTT	AGCAAAAGCG	3660
TCCAGAGAGG	AGAGCTTAGC	AGGAGTCCTA	GCCCTTTCAC	CCATACACAT	TTGGCTCAGG	3720
GTTACCGAAG	AGGGGCCAAG	AAATTAGAGT	CCTCAGAAGA	GAAC TTATCT	AGTGAGGATG	3780
AAGAGCTTCC	CTGCTTCCAA	CACTTGTTAT	TTGGTAAAGT	AAACAATATA	CCTTCTCAGT	3840
CTACTAGGCA	TAGCACC GTT	GCTACCGAGT	GTCTGTCTAA	GAACACAGAG	GAGAATTTAT	3900
TATCATTGAA	GAATAGCTTA	AATGACTGCA	GTAACCAGGT	AATATTGGCA	AAGGCATCTC	3960
AGGAACATCA	CCTTAGTGAG	GAAACAAAAT	GTTCTGCTAG	CTTGTTTTCT	TCACAGTGCA	4020
GTGAATTGGA	AGACTTGACT	GCAAATACAA	ACACCCAGGA	TCCTTTCTTG	ATTGGTTCTT	4080
CCAAACAAAT	GAGGCATCAG	TCTGAAAGCC	AGGGAGTTGG	TCTGAGTGAC	AAGGAATTGG	4140
TTTCAGATGA	TGAAGAAAGA	GGAACGGGCT	TGGAAGAAAA	TAATCAAGAA	GAGCAAAGCA	4200
TGGATTCAAA	CTTAGGTGAA	GCAGCATCTG	GGTGTGAGAG	TGAAACAAGC	GTCTCTGAAG	4260
ACTGCTCAGG	GCTATCCTCT	CAGAGTGACA	TTTTAACCAC	TCAGCAGAGG	GATACCATGC	4320
AACATAACCT	GATAAAGCTC	CAGCAGGAAA	TGGCTGAACT	AGAAGCTGTG	TTAGAACAGC	4380
ATGGGAGCCA	GCCTTCTAAC	AGCTACCCTT	CCATCATAAG	TGACTCTTCT	GCCCTTGAGG	4440
ACCTGCGAAA	TCCAGAACAA	AGCACATCAG	AAAAAGCAGT	ATTA ACTTCA	CAGAAAAGTA	4500
GTGAATACCC	TATAAGCCAG	AATCCAGAAG	GCCTTTCTGC	TGACAAGTTT	GAGGTGTCTG	4560
CAGATAGTTC	TACCAGTAAA	AATAAAGAAC	CAGGAGTGGA	AAGGTCATCC	CCTTCTAAAT	4620
GCCCATCATT	AGATGATAGG	TGGTACATGC	ACAGTTGCTC	TGGGAGTCTT	CAGAATAGAA	4680
ACTACCCATC	TCAAGAGGAG	CTCATTAAGG	TTGTTGATGT	GGAGGAGCAA	CAGCTGGAAG	4740
AGTCTGGGCC	ACACGATTTG	ACGGAAACAT	CTTACTTGCC	AAGGCAAGAT	CTAGAGGGAA	4800

CCCCTTACCT GGAATCTGGA ATCAGCCTCT TCTCTGATGA CCCTGAATCT GATCCTTCTG	4860
AAGACAGAGC CCCAGAGTCA GCTCGTGTTG GCAACATACC ATCTTCAACC TCTGCATTGA	4920
AAGTTCCCCA ATTGAAAGTT GCAGAATCTG CCCAGGGTCC AGCTGCTGCT CATACTACTG	4980
ATACTGCTGG GTATAATGCA ATGGAAGAAA GTGTGAGCAG GGAGAAGCCA GAATTGACAG	5040
CTTCAACAGA AAGGGTCAAC AAAAGAATGT CCATGGTGGT GTCTGGCCTG ACCCCAGAAG	5100
AATTTATGCT CGTGTACAAG TTTGCCAGAA AACACCACAT CACTTTAACT AATCTAATTA	5160
CTGAAGAGAC TACTCATGTT GTTATGAAAA CAGATGCTGA GTTTGTGTGT GAACGGACAC	5220
TGAAATATTT TCTAGGAATT GCGGGAGGAA AATGGGTAGT TAGCTATTTC TGGGTGACCC	5280
AGTCTATTAA AGAAAGAAAA ATGCTGAATG AGCATGATTT TGAAGTCAGA GGAGATGTGG	5340
TCAATGGAAG AAACCACCAA GGTCCAAAGC GAGCAAGAGA ATCCCAGGAC AGAAAGATCT	5400
TCAGGGGGCT AGAAATCTGT TGCTATGGGC CCTTCACCAA CATGCCCACA GATCAACTGG	5460
AATGGATGGT ACAGCTGTGT GGTGCTTCTG TGGTGAAGGA GCTTTCATCA TTCACCCTTG	5520
GCACAGGTGT CCACCCAATT GTGGTTGTGC AGCCAGATGC CTGGACAGAG GACAATGGCT	5580
TCCATGCAAT TGGGCAGATG TGTGAGGCAC CTGTGGTGAC CCGAGAGTGG GTGTTGGACA	5640
GTGTAGCACT CTACCAGTGC CAGGAGCTGG ACACCTACCT GATACCCAG ATCCCCACA	5700
GCCACTACTG A	5711

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1863 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

- (ii) MOLECULE TYPE: protein
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens  
 (B) STRAIN: BRCA1
- (viii) POSITION IN GENOME:  
 (A) CHROMOSOME/SEGMENT: 17  
 (B) MAP POSITION: 17q21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asp	Leu	Ser	Ala	Leu	Arg	Val	Glu	Glu	Val	Gln	Asn	Val	Ile	Asn	1	5	10	15
Ala	Met	Gln	Lys	Ile	Leu	Glu	Cys	Pro	Ile	Cys	Leu	Glu	Leu	Ile	Lys	20	25	30	
Glu	Pro	Val	Ser	Thr	Lys	Cys	Asp	His	Ile	Phe	Cys	Lys	Phe	Cys	Met	35	40	45	
Leu	Lys	Leu	Leu	Asn	Gln	Lys	Lys	Gly	Pro	Ser	Gln	Cys	Pro	Leu	Cys	50	55	60	
Lys	Asn	Asp	Ile	Thr	Lys	Arg	Ser	Leu	Gln	Glu	Ser	Thr	Arg	Phe	Ser	65	70	75	80
Gln	Leu	Val	Glu	Glu	Leu	Leu	Lys	Ile	Ile	Cys	Ala	Phe	Gln	Leu	Asp	85	90	95	
Thr	Gly	Leu	Glu	Tyr	Ala	Asn	Ser	Tyr	Asn	Phe	Ala	Lys	Lys	Glu	Asn	100	105	110	
Asn	Ser	Pro	Glu	His	Leu	Lys	Asp	Glu	Val	Ser	Ile	Ile	Gln	Ser	Met	115	120	125	
Gly	Tyr	Arg	Asn	Arg	Ala	Lys	Arg	Leu	Leu	Gln	Ser	Glu	Pro	Glu	Asn	130	135	140	

Pro Ser Leu Gln Glu Thr Ser Leu Ser-Val Gln Leu Ser Asn Leu Gly  
 145 150 155 160  
 Thr Val Arg Thr Leu Arg Thr Lys Gln Arg Ile Gln Pro Gln Lys Thr  
 165 170 175  
 Ser Val Tyr Ile Glu Leu Gly Ser Asp Ser Ser Glu Asp Thr Val Asn  
 180 185 190  
 Lys Ala Thr Tyr Cys Ser Val Gly Asp Gln Glu Leu Leu Gln Ile Thr  
 195 200 205  
 Pro Gln Gly Thr Arg Asp Glu Ile Ser Leu Asp Ser Ala Lys Lys Ala  
 210 215 220  
 Ala Cys Glu Phe Ser Glu Thr Asp Val Thr Asn Thr Glu His His Gln  
 225 230 235 240  
 Pro Ser Asn Asn Asp Leu Asn Thr Thr Glu Lys Arg Ala Ala Glu Arg  
 245 250 255  
 His Pro Glu Lys Tyr Gln Gly Ser Ser Val Ser Asn Leu His Val Glu  
 260 265 270  
 Pro Cys Gly Thr Asn Thr His Ala Ser Ser Leu Gln His Glu Asn Ser  
 275 280 285  
 Ser Leu Leu Leu Thr Lys Asp Arg Met Asn Val Glu Lys Ala Glu Phe  
 290 295 300  
 Cys Asn Lys Ser Lys Gln Pro Gly Leu Ala Arg Ser Gln His Asn Arg  
 305 310 315 320  
 Trp Ala Gly Ser Lys Glu Thr Cys Asn Asp Arg Arg Thr Pro Ser Thr  
 325 330 335  
 Glu Lys Lys Val Asp Leu Asn Ala Asp Pro Leu Cys Glu Arg Lys Glu  
 340 345 350

Trp Asn Lys Gln Lys Leu Pro Cys Ser Glu Asn Pro Arg Asp Thr Glu  
 355 360 365  
 Asp Val Pro Trp Ile Thr Leu Asn Ser Ser Ile Gln Lys Val Asn Glu  
 370 375 380  
 Trp Phe Ser Arg Ser Asp Glu Leu Leu Gly Ser Asp Asp Ser His Asp  
 385 390 395 400  
 Gly Glu Ser Glu Ser Asn Ala Lys Val Ala Asp Val Leu Asp Val Leu  
 405 410 415  
 Asn Glu Val Asp Glu Tyr Ser Gly Ser Ser Glu Lys Ile Asp Leu Leu  
 420 425 430  
 Ala Ser Asp Pro His Glu Ala Leu Ile Cys Lys Ser Glu Arg Val His  
 435 440 445  
 Ser Lys Ser Val Glu Ser Asn Ile Glu Asp Lys Ile Phe Gly Lys Thr  
 450 455 460  
 Tyr Arg Lys Lys Ala Ser Leu Pro Asn Leu Ser His Val Thr Glu Asn  
 465 470 475 480  
 Leu Ile Ile Gly Ala Phe Val Thr Glu Pro Gln Ile Ile Gln Glu Arg  
 485 490 495  
 Pro Leu Thr Asn Lys Leu Lys Arg Lys Arg Arg Pro Thr Ser Gly Leu  
 500 505 510  
 His Pro Glu Asp Phe Ile Lys Lys Ala Asp Leu Ala Val Gln Lys Thr  
 515 520 525  
 Pro Glu Met Ile Asn Gln Gly Thr Asn Gln Thr Glu Gln Asn Gly Gln  
 530 535 540  
 Val Met Asn Ile Thr Asn Ser Gly His Glu Asn Lys Thr Lys Gly Asp  
 545 550 555 560  
 Ser Ile Gln Asn Glu Lys Asn Pro Asn Pro Ile Glu Ser Leu Glu Lys





Leu Leu Glu Val Ser Thr Leu Gly Lys Ala Lys Thr Glu Pro Asn Lys  
 785 790 795 800  
 Cys Val Ser Gln Cys Ala Ala Phe Glu Asn Pro Lys Gly Leu Ile His  
 805 810 815  
 Gly Cys Ser Lys Asp Asn Arg Asn Asp Thr Glu Gly Phe Lys Tyr Pro  
 820 825 830  
 Leu Gly His Glu Val Asn His Ser Arg Glu Thr Ser Ile Glu Met Glu  
 835 840 845  
 Glu Ser Glu Leu Asp Ala Gln Tyr Leu Gln Asn Thr Phe Lys Val Ser  
 850 855 860  
 Lys Arg Gln Ser Phe Ala Leu Phe Ser Asn Pro Gly Asn Ala Glu Glu  
 865 870 875 880  
 Glu Cys Ala Thr Phe Ser Ala His Ser Gly Ser Leu Lys Lys Gln Ser  
 885 890 895  
 Pro Lys Val Thr Phe Glu Cys Glu Gln Lys Glu Glu Asn Gln Gly Lys  
 900 905 910  
 Asn Glu Ser Asn Ile Lys Pro Val Gln Thr Val Asn Ile Thr Ala Gly  
 915 920 925  
 Phe Pro Val Val Gly Gln Lys Asp Lys Pro Val Asp Asn Ala Lys Cys  
 930 935 940  
 Ser Ile Lys Gly Gly Ser Arg Phe Cys Leu Ser Ser Gln Phe Arg Gly  
 945 950 955 960  
 Asn Glu Thr Gly Leu Ile Thr Pro Asn Lys His Gly Leu Leu Gln Asn  
 965 970 975  
 Pro Tyr Arg Ile Pro Pro Leu Phe Pro Ile Lys Ser Phe Val Lys Thr  
 980 985 990  
 Lys Cys Lys Lys Asn Leu Leu Glu Glu Asn Phe Glu Glu His Ser Met  
 995 1000 1005

Ser Pro Glu Arg Glu Met Gly Asn Glu Asn Ile Pro Ser Thr Val Ser  
 1010 1015 1020  
 Thr Ile Ser Arg Asn Asn Ile Arg Glu Asn Val Phe Lys Gly Ala Ser  
 1025 1030 1035 1040  
 Ser Ser Asn Ile Asn Glu Val Gly Ser Ser Thr Asn Glu Val Gly Ser  
 1045 1050 1055  
 Ser Ile Asn Glu Ile Gly Ser Ser Asp Glu Asn Ile Gln Ala Glu Leu  
 1060 1065 1070  
 Gly Arg Asn Arg Gly Pro Lys Leu Asn Ala Met Leu Arg Leu Gly Val  
 1075 1080 1085  
 Leu Gln Pro Glu Val Tyr Lys Gln Ser Leu Pro Gly Ser Asn Cys Lys  
 1090 1095 1100  
 His Pro Glu Ile Lys Lys Gln Glu Tyr Glu Glu Val Val Gln Thr Val  
 1105 1110 1115 1120  
 Asn Thr Asp Phe Ser Pro Tyr Leu Ile Ser Asp Asn Leu Glu Gln Pro  
 1125 1130 1135  
 Met Gly Ser Ser His Ala Ser Gln Val Cys Ser Glu Thr Pro Asp Asp  
 1140 1145 1150  
 Leu Leu Asp Asp Gly Glu Ile Lys Glu Asp Thr Ser Phe Ala Glu Asn  
 1155 1160 1165  
 Asp Ile Lys Glu Ser Ser Ala Val Phe Ser Lys Ser Val Gln Arg Gly  
 1170 1175 1180  
 Glu Leu Ser Arg Ser Pro Ser Pro Phe Thr His Thr His Leu Ala Gln  
 1185 1190 1195 1200  
 Gly Tyr Arg Arg Gly Ala Lys Lys Leu Glu Ser Ser Glu Glu Asn Leu  
 1205 1210 1215  
 Ser Ser Glu Asp Glu Glu Leu Pro Cys Phe Gln His Leu Leu Phe Gly

85

Asp Leu Arg Asn Pro Glu Gln Ser Thr-Ser Glu Lys Ala Val Leu Thr  
 1445 1450 1455  
 Ser Gln Lys Ser Ser Glu Tyr Pro Ile Ser Gln Asn Pro Glu Gly Leu  
 1460 1465 1470  
 Ser Ala Asp Lys Phe Glu Val Ser Ala Asp Ser Ser Thr Ser Lys Asn  
 1475 1480 1485  
 Lys Glu Pro Gly Val Glu Arg Ser Ser Pro Ser Lys Cys Pro Ser Leu  
 1490 1495 1500  
 Asp Asp Arg Trp Tyr Met His Ser Cys Ser Gly Ser Leu Gln Asn Arg  
 1505 1510 1515 1520  
 Asn Tyr Pro Ser Gln Glu Glu Leu Ile Lys Val Val Asp Val Glu Glu  
 1525 1530 1535  
 Gln Gln Leu Glu Glu Ser Gly Pro His Asp Leu Thr Glu Thr Ser Tyr  
 1540 1545 1550  
 Leu Pro Arg Gln Asp Leu Glu Gly Thr Pro Tyr Leu Glu Ser Gly Ile  
 1555 1560 1565  
 Ser Leu Phe Ser Asp Asp Pro Glu Ser Asp Pro Ser Glu Asp Arg Ala  
 1570 1575 1580  
 Pro Glu Ser Ala Arg Val Gly Asn Ile Pro Ser Ser Thr Ser Ala Leu  
 1585 1590 1595 1600  
 Lys Val Pro Gln Leu Lys Val Ala Glu Ser Ala Gln Gly Pro Ala Ala  
 1605 1610 1615  
 Ala His Thr Thr Asp Thr Ala Gly Tyr Asn Ala Met Glu Glu Ser Val  
 1620 1625 1630  
 Ser Arg Glu Lys Pro Glu Leu Thr Ala Ser Thr Glu Arg Val Asn Lys  
 1635 1640 1645

Arg Met Ser Met Val Val Ser Gly Leu Thr Pro Glu Glu Phe Met Leu  
 1650 1655 1660  
 Val Tyr Lys Phe Ala Arg Lys His His Ile Thr Leu Thr Asn Leu Ile  
 1665 1670 1675 1680  
 Thr Glu Glu Thr Thr His Val Val Met Lys Thr Asp Ala Glu Phe Val  
 1685 1690 1695  
 Cys Glu Arg Thr Leu Lys Tyr Phe Leu Gly Ile Ala Gly Gly Lys Trp  
 1700 1705 1710  
 Val Val Ser Tyr Phe Trp Val Thr Gln Ser Ile Lys Glu Arg Lys Met  
 1715 1720 1725  
 Leu Asn Glu His Asp Phe Glu Val Arg Gly Asp Val Val Asn Gly Arg  
 1730 1735 1740  
 Asn His Gln Gly Pro Lys Arg Ala Arg Glu Ser Gln Asp Arg Lys Ile  
 1745 1750 1755 1760  
 Phe Arg Gly Leu Glu Ile Cys Cys Tyr Gly Pro Phe Thr Asn Met Pro  
 1765 1770 1775  
 Thr Asp Gln Leu Glu Trp Met Val Gln Leu Cys Gly Ala Ser Val Val  
 1780 1785 1790  
 Lys Glu Leu Ser Ser Phe Thr Leu Gly Thr Gly Val His Pro Ile Val  
 1795 1800 1805  
 Val Val Gln Pro Asp Ala Trp Thr Glu Asp Asn Gly Phe His Ala Ile  
 1810 1815 1820  
 Gly Gln Met Cys Glu Ala Pro Val Val Thr Arg Glu Trp Val Leu Asp  
 1825 1830 1835 1840  
 Ser Val Ala Leu Tyr Gln Cys Gln Glu Leu Asp Thr Tyr Leu Ile Pro  
 1845 1850 1855  
 Gln Ile Pro His Ser His Tyr  
 1860



0973672 032602

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
  - (B) STRAIN: 2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAAGTTGTCA TTTTATAAAC CTTT

24

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
  - (B) STRAIN: 2R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGTCTTTTCT TCCCTAGTAT GT

22

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 3F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TCCTGACACA GCAGACATTT A

2:

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 3R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTGGATTTTC GTTCTCACTT A

21:

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 5F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTCTTAAGGG CAGTTGTGAG

20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 5R-M13\* primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTCCTACTGT GGTGCTTCC

20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 6/7F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTTATTTTAG TGTCCTTAAA AGG

2

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 6R

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTCATGGAC AGCACTTGAG TG

22

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 7F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CACAACAAAG AGCATACATA GGG

23

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 6/7R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TCGGGTTCAC TCTGTAGAAG

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 8F1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTCTCTTCAG GAGGAAAAGC A

21

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 8R1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCTGCCTACC ACAAATACAA A

21

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 9F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCACAGTAGA TGCTCAGTAA ATA

23

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 9R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TAGGAAAATA CCAGCTTCAT AGA

23

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 10F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGGTCAGCTT TCTGTAATCG

2

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 10R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATCTACCC ACTCTCTTCT TCAG

24

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11AF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCACCTCCAA GGTGTATCA

19

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11AR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGTTATGTTG GCTCCTTGCT

20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11BF1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CACTAAAGAC AGAATGAATC TA

22

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 11BR1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAAGAACCAG AATATTCATC TA

22

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 11CF1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGATGGGGAG TCTGAATCAA

2

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 11CR1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TCTGCTTTCT TGATAAAATC CT

22

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 11DF1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGCGTCCCCT CACAAATAAA

20



## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (B) STRAIN: 11DR1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TCAAGCGCAT GAATATGCCT

20

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (B) STRAIN: 11EF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTATAAGCAA TATGGAATC GA

22

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 11ER primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTAAGTTCACT GGTATTTGAA CA

23

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 11FF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GACAGCGATA CTTTCCCAGA

20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11FR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TGGAACAACC ATGAATTAGT C

21

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11GF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGAAGTTAGC ACTCTAGGGA

20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11GR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GCAGTGATAT TAACTGTCTG TA

22

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11HF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TGGGTCCTTA AAGAAACAAA GT

22

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11HR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TCAGGTGACA TTGAATCTTC C

21

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11IF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CCACTTTTTTC CCATCAAGTC A

21

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11IR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TCAGGATGCT TACAATTACT TC

22

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11JF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CAAAATTGAA TGCTATGCTT AGA

23

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11JR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCGGTAACCC TGAGCCAAAT

21

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 11KF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GCAAAAGCGT CCAGAAAGGA

20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 11KR-1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TATTTGCAGT CAAGTCTTCC AA

22

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 11LF-1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GTAATATTGG CAAAGGCATC T

21

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 11LR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TAAAATGTGC TCCCCAAAAG CA

22



(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 12F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTCCTGCCAA TGAGAAGAAA

20

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 12R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TGTCAGCAAA CCTAAGAATG T

21

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 14F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTAACCTGAA TTATCACTAT CA

22

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 14R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GTGTATAAAT GCCTGTATGC A

21

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 15F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGGCTGCCCA GGAAGTATG

19

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 15R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

AACCAGAATA TCTTTATGTA GGA

23

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
(B) STRAIN: 16F primer

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

AATTCTTAAC AGAGACCAGA AC

22

- (2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
(B) STRAIN: 16R primer

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

AAAACCTCTTT CCAGAATGTT GT

22

- (2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
(B) STRAIN: 17F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GTGTAGAACG TGCAGGATTG

20

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 17R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TCGCCTCATG TGGTTTTA

18

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 18F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGCTCTTTAG CTTCTTAGGA C

21

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 18R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GAGACCATT TCCCAGCATC

20

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 19F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CTGTCATTCT TCCTGTGCTC

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GTGTAGAACG TGCAGGATTG

20

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 17R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TCGCCTCATG TGGTTTTA

18

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 18F primer



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 20R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GGGAATCCAA ATTACACAGC

20

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 21F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

AAGCTCTTCC TTTTGTAAAG TC

22

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 21R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GTAGAGAAAT AGAATAGCCT CT

22

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 22F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

TCCCATGAG AGGTCTTGCT

20

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 22R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GAGAAGACTT CTGAGGCTAC

20

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 23F-1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

TGAAGTGACA GTTCCAGTAG T

21

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 23R-1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CATTTTAGCC ATTCATTCAA CAA

23

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 24F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ATGAATTGAC ACTAATCTCT GC

22

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 24R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GTAGCCAGGA CAGTAGAAGG A

21

B